

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: Yoram Reiter
- (ii) TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES, CONSTRUCTS ENCODING SAME AND METHODS OF GENERATING SAME
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
- (B) STREET: 2001 Jefferson Davis Highway, Suite 207
- (C) CITY: Arlington
- (D) STATE: Virginia
- (E) COUNTRY: United States of America
- (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
- (B) COMPUTER: Twinhead* Slimnote-890TX
- (C) OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
- (D) SOFTWARE: Word for Windows version 2.0 converted to
an ASCII file
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Friedmam, Mark M.
- (B) REGISTRATION NUMBER: 33,883
- (C) REFERENCE/DOCKET NUMBER: 74/92
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 972-3-5625553
- (B) TELEFAX: 972-3-5625554
- (C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
Ile Met Asp Gln Val Pro Phe Ser Val
- 5
- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
Tyr Leu Glu Pro Gly Pro Val Thr Val
- 5
- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
Leu Leu Phe Gly Tyr Pro Val Tyr Val
- 5
- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1248
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
ATGATCCAGC GTACTCCAAA GATTCAAGGT TACTCACGTC ATCCAGCAGA 50
GAATGGAAAG TCAAATTCTC TGAATTGCTA TGTTGCTGGG TTTCATCCAT 100
CCGACATTGA AGTTGACTTA CTGAAGAATG GAGAGAGAAT TGAAAAAGTG 150
GAGCATTCAAGCTTGTCTT CAGCAAGGAC TGTTCTTCT ATCTCTTGTA 200
TTATACTGAG TTCACCCCCA CTGAAAAAGA TGAGTATGCC TGCCGTGTGA 250

ACCACTGTGAC	TTTGTACAG	CCCAAGATAG	TTAACGTGGGA	TGCGAGACATG	300
GGTGCGGGTG	GAAGCGGCGG	TGGAGGCCTCT	GGTGGAGGTG	GCAGCGGCCTC	350
TCACTCCATG	AGGTATTTCT	TCACATCCGT	GTCCCCGCC	GGCCGCGGGG	400
AGCCCCGCTT	CATCGCAGTG	GGCTACATGG	ACGACACGCA	TTGTCGCGG	450
TTCGACAGCG	ACGCCCGGAG	CCAGAGGATG	GAGCCGCGGG	CGCCGTGGAT	500
AGAGCAGGGAG	GGTCGGAGT	ATTGGGACGG	GGAGACACGG	AAAGTGAAGG	550
CCCACACTACA	GACTCACCGA	GTGGACCTGG	GGACCCCTGC	CGGCTACTAC	600
AACACAGAGCC	GGCCCGGTT	TCACACCGTC	CAGAGGATGT	ATGGCTGCGA	650
CGTGGGGTCTG	GACTGGCGCT	TCCTCCGCGG	GTACCACCA	TACGCCCTACG	700
ACGCCAAGGA	TTACATCGCC	CTGAAAGAGG	ACTGCGCTC	TTGGACCCGCG	750
GCGGACATGG	CAGCTCACAG	CACCAAGCAC	ATACTGGGAGG	CGGGCCATATG	800
GGCCGGACGAC	TTGAGAGGCC	ACCTGGAGGG	CACGTGCGTG	GAGTGGCTCC	850
GCAGATACCT	GGAGAACCGG	AAGGAGACGC	TGCAGCCGAC	GGACGCCCGCC	900
AAAACCGCCA	TGACTCTACCA	CCTGCTCTCT	GACCATGAAG	CCACCCCTGAG	950
GTGCTGGGGC	CTGAGCTCT	ACCTGGCGGA	GATCACACTG	ACCTGGCAGC	1000
GGACTTGGAG	GAATCTTGA	GGCAATGAAG	ATGGAGCTGC	GGGACTGA	1248

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ile	Gln	Arg	Thr	Pro	Lys	Ile	Gln	Val	Tyr	Ser	Arg	His	Pro
					5				10					15
Ala	Glu	Asn	Gly	Lys	Ser	Asn	Phe	Leu	Asn	Cys	Tyr	Val	Ser	Gly
				20					25					30
Phe	His	Pro	Ser	Asp	Ile	Glu	Val	Asp	Leu	Leu	Lys	Asn	Gly	Glu
				35					40					45
Arg	Ile	Glu	Lys	Val	Glu	His	Ser	Asp	Leu	Ser	Phe	Ser	Lys	Asp
				50					55					60
Trp	Ser	Phe	Tyr	Leu	Leu	Tyr	Tyr	Thr	Glu	Phe	Thr	Pro	Thr	Glu
				65					70					75
Lys	Asp	Glu	Tyr	Ala	Cys	Arg	Val	Asn	His	Val	Thr	Leu	Ser	Gln
				80					85					90
Pro	Lys	Ile	Val	Lys	Trp	Asp	Arg	Asp	Met	Gly	Gly	Gly	Ser	
				95					100					105
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	His	Ser	Met
				110					115					120
Arg	Tyr	Phe	Phe	Thr	Ser	Val	Ser	Arg	Pro	Gly	Arg	Gly	Glu	Pro
				125					130					135
Arg	Phe	Ile	Ala	Val	Gly	Tyr	Val	Asp	Asp	Thr	Gln	Phe	Val	Arg
				140					145					150
Phe	Asp	Ser	Asp	Ala	Ala	Ser	Gln	Arg	Met	Glu	Pro	Arg	Ala	Pro
				155					160					165
Trp	Ile	Glu	Gln	Glu	Gly	Pro	Glu	Tyr	Trp	Asp	Gly	Glu	Thr	Arg
				170					175					180
Lys	Val	Lys	Ala	His	Ser	Gln	Thr	His	Arg	Val	Asp	Leu	Gly	Thr
				185					190					195
Leu	Arg	Gly	Tyr	Tyr	Asn	Gln	Ser	Glu	Ala	Gly	Ser	His	Thr	Val
				200					205					210
Gln	Arg	Met	Tyr	Gly	Cys	Asp	Val	Gly	Ser	Asp	Trp	Arg	Phe	Leu
				215					220					225
Arg	Gly	Tyr	His	Gln	Tyr	Ala	Tyr	Asp	Gly	Lys	Asp	Tyr	Ile	Ala
				230					235					240
Leu	Lys	Glu	Asp	Leu	Arg	Ser	Trp	Thr	Ala	Ala	Asp	Met	Ala	Ala
				245					250					255
Gln	Thr	Thr	Lys	His	Lys	Trp	Glu	Ala	Ala	His	Val	Ala	Glu	Gln
				260					265					270
Leu	Arg	Ala	Tyr	Leu	Glu	Gly	Thr	Cys	Val	Glu	Trp	Leu	Arg	Arg
				275					280					285
Tyr	Leu	Glu	Asn	Gly	Lys	Glu	Thr	Leu	Gln	Arg	Thr	Asp	Ala	Pro
				290					295					300
Lys	Thr	His	Met	Thr	His	His	Ala	Val	Ser	Asp	His	Glu	Ala	Thr
				305					310					315
Leu	Arg	Cys	Trp	Ala	Leu	Ser	Phe	Tyr	Pro	Ala	Glu	Ile	Thr	Leu
				320					325					330
Thr	Trp	Gln	Arg	Asp	Gly	Glu	Asp	Gln	Thr	Gln	Asp	Thr	Glu	Leu
				335					340					345
Val	Glu	Thr	Arg	Pro	Ala	Gly	Asp	Gly	Thr	Phe	Gln	Lys	Trp	Ala
				350					355					360
Ala	Val	Val	Val	Pro	Ser	Gly	Gln	Glu	Gln	Arg	Tyr	Thr	Cys	His
				365					370					375
Val	Gln	His	Glu	Gly	Leu	Pro	Lys	Pro	Leu	Thr	Leu	Arg	Trp	Glu
				380					385					390
Gln	Ser	Thr	Arg	Gly	Gly	Ala	Ser	Gly	Gly	Gly	Leu	Gly	Gly	Ile
				395					400					405
Phe	Glu	Ala	Met	Lys	Met	Glu	Leu	Arg	Asp					
				410					415					

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Ser His Ser Met Arg Tyr Phe Thr Ser Val Ser Arg Pro
 5 10 15
 Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp
 20 25 30
 Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met
 35 40 45
 Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp
 50 55 60
 Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His Arg
 65 70 75
 Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala
 80 85 90
 Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser
 95 100 105
 Asp Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly
 110 115 120
 Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala
 125 130 135
 Ala Asp Met Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala
 140 145 150
 His Val Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val
 155 160 165
 Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln
 170 175 180
 Arg Thr Asp Ala Pro Lys Thr His Met Thr His His Ala Val Ser
 185 190 195
 Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro
 200 205 210
 Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr
 215 220 225
 Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
 230 235 240
 Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln
 245 250 265
 Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu
 270 275 280
 Thr Leu Arg Trp Glu Gln Ser Thr Arg Gly
 285 290

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro
 5 10 15
 Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly
 20 25 30
 Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu
 35 40 45
 Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp
 50 55 60
 Trp Ser Phe Tyr Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu
 65 70 75
 Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln
 80 85 90
 Pro Lys Ile Val Lys Trp Asp Arg Asp Met
 95 100

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGAGATATA CATATGGGCT CTCACTCCAT GAGGTA 36

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 CGGGCTTTGT TAGCACCGAT TCATAGGTGA GGGGCTTGGG CAA 43

(2) INFORMATION FOR SEQ ID NO:10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
 GGAGATATACT ATATGATCCA GCGTACTCCA AAGAT 35

(2) INFORMATION FOR SEQ ID NO:12:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
 CGGGCTTTGT TAGCAGCCGA ATTCAATTACA TGTCCTCGATC CCACTAAC 49

(2) INFORMATION FOR SEQ ID NO:13:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
 GGAAGGCGTT GGCAGCATATG ATCCAGCGTA CTCCAAAGAT T 41

(2) INFORMATION FOR SEQ ID NO:14:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
 GGAAGCGGGCG GTGGAGGCTC TGGTGGAGGT GGCAGCGGCT CTCACTCCAT 50
 GA 52

(2) INFORMATION FOR SEQ ID NO:15:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
 GGAAGCGGGCG GTGGAGGCTC TGGTGGAGGT GGCAGCGGCT CTCACTCCAT 50
 GA 52

(2) INFORMATION FOR SEQ ID NO:16:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
 GGGAGAATTCTTACTCCCCAT CTCAGGGTGA GGGGCTTGGG CAA 43

(2) INFORMATION FOR SEQ ID NO:17:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
 Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp

(2) INFORMATION FOR SEQ ID NO:19:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
CACTAAAGC TTTTATTCAG CCTCCGAAC GTGGATGCCT CCACGCGGAA 50
CCTCCACCGA AACCCACTCC GGACCCGCCA CCTCCCTCCC ATCTCAGGGT 100

(2) INFORMATION FOR SEQ ID NO:20:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
GGAATCTTGT AGGCAATGAA GATGGAGCTG CGGGACTGA 39